SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rng.

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This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rng.

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```
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OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 13:36:04 ; Search time 1314 Seconds
                                          (without alignments)
                            11105.720 Million cell updates/sec

Title:         US-10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:     10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     N_Geneseq_8:*
               1:  geneseqn1980s:*
               2:  geneseqn1990s:*
               3:  geneseqn2000s:*
               4:  geneseqn2001as:*
               5:  geneseqn2001bs:*
               6:  geneseqn2002as:*
               7:  geneseqn2002bs:*
               8:  geneseqn2003as:*
               9:  geneseqn2003bs:*
               10: geneseqn2003cs:*
               11: geneseqn2003ds:*
               12: geneseqn2004as:*
               13: geneseqn2004bs:*
               14: geneseqn2005s:*
               15: geneseqn2006s:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2093	100.0	2093	10	ADF90163	Adf90163 cDNA enco
2	2093	100.0	2093	13	ADR03798	Adr03798 Human cDN
3	1847.6	88.3	2057	8	ABZ80236	Abz80236 Human tra
4	1806.4	86.3	5821	14	ADZ49865	Adz49865 Insulin s
5	1806	86.3	2807	8	ABX12019	Abx12019 Transport
6	1609.8	76.9	3114	6	AAL44674	Aal44674 Human tra
7	1541.8	73.7	1961	10	ADA53869	Ada53869 Human cod
8	1541.8	73.7	1961	13	ADS10331	Ads10331 Human the
9	1498.4	71.6	1597	8	ABX70783	Abx70783 Novel hum
10	1441.8	68.9	1501	10	ABX70643	Abx70643 Human cDN
11	1363.8	65.2	1513	10	ABX70642	Abx70642 Human cDN
12	1327.2	63.4	1428	4	ABL57930	Abl57930 Human VG5
13	1133	54.1	1784	4	ABL57913	Abl57913 Rat VG51

```
┌─────────────────────────────────────────────────────────────────┐
│                                                                   │
│      SCORE Search Results Details for Application                 │
│      10679362 and Search Result us-10-679-362-                    │
│                          1.rge.                                   │
│                                                                   │
└─────────────────────────────────────────────────────────────────┘
```

Score Home   Retrieve Application   SCORE System   SCORE   Comments /
Page   List   Overview   FAQ   Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rge.

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```
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OM nucleic - nucleic search, using sw model

Run on:         August  7, 2006, 13:37:36 ; Search time 19131 Seconds
                                             (without alignments)
                                             6996.077 Million cell updates/sec

Title:          US-10-679-362-1
Perfect score:  2093
Sequence:       1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
                10: gb_vi:*
                11: gb_ov:*
                12: gb_htg:*
                13: gb_in:*
                14: gb_om:*
                15: gb_ba:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result           Query
No.      Score   Match Length DB  ID                  Description
-------------------------------------------------------------------------
     1    1806    86.3   5823  5   HSM806092           BX537963 Homo sapi
     2    1791.6  85.6   5585  5   AF516142            AF516142 Homo sapi
     3    1691.2  80.8   2028  5   AB168788            AB168788 Macaca fa
     4    1609.8  76.9   3114  2   AX686980            AX686980 Sequence
     5    1585.4  75.7   1710  5   AY162213            AY162213 Homo sapi
     6    1541.8  73.7   1961  2   AX714753            AX714753 Sequence
     7    1541.8  73.7   1961  5   AK057340            AK057340 Homo sapi
     8    1498.4  71.6   1597  2   AR541761            AR541761 Sequence
     9    1498.4  71.6   1597  2   AR698923            AR698923 Sequence
    10    1441.8  68.9   1501  2   AX717763            AX717763 Sequence
    11    1370    65.5   2296  14  AY989816            AY989816 Oryctolag
    12    1363.8  65.2   1513  2   AX717761            AX717761 Sequence
    13    1327.2  63.4   1428  2   AX049362            AX049362 Sequence
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rst.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rst.

start

```
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OM nucleic - nucleic search, using sw model

Run on:        August  7, 2006, 13:56:43 ; Search time 9987 Seconds
                                           (without alignments)
                               11719.151 Million cell updates/sec

Title:         US-10-679-362-1
Perfect score: 2093
Sequence:      1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:      96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     EST:*
               1:  gb_est1:*
               2:  gb_est3:*
               3:  gb_est4:*
               4:  gb_est5:*
               5:  gb_est6:*
               6:  gb_htc:*
               7:  gb_est2:*
               8:  gb_est7:*
               9:  gb_est8:*
               10: gb_est9:*
               11: gb_gss1:*
               12: gb_gss2:*
               13: gb_gss3:*
               14: gb_gss4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result          Query
No.     Score   Match Length DB  ID                  Description
-------------------------------------------------------------------------------
     1   1266    60.5  1482  14  DQ050191            DQ050191 Homo sapi
     2   1235.6  59.0  1481  14  DQ050192            DQ050192 Pan trogl
     3   867.6   41.5  3404   6  CR859927            CR859927 Pongo pyg
     4   833.6   39.8  2412   6  AK156409            AK156409 Mus muscu
     5   833.6   39.8  2422   6  AK041041            AK041041 Mus muscu
     6   832     39.8  1632   6  AK160394            AK160394 Mus muscu
     7   832     39.8  2371   6  AK079053            AK079053 Mus muscu
     8   707.2   33.8   790   1  AL043182            AL043182 DKFZp434G
     9   638.4   30.5  2481  14  DQ039367            DQ039367 Homo sapi
    10   623.6   29.8  1844   6  AK132910            AK132910 Mus muscu
    11   614.4   29.4   632   3  BM696484            BM696484 UI-E-DWO-
    12   605.6   28.9  2475  14  DQ039368            DQ039368 Pan trogl
    13   601.6   28.7  1280   5  CJ105223            CJ105223 CJ105223
    14   582.8   27.8   747   5  CK634094            CK634094 UI-M-HNO-
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-1.rni.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-1.rni.

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```
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OM nucleic - nucleic search, using sw model

Run on:          August  7, 2006, 13:58:37 ; Search time 416 Seconds
                                             (without alignments)
                                             9414.016 Million cell updates/sec

Title:           US-10-679-362-1
Perfect score:   2093
Sequence:        1 cgggcagcaaaggaggatgg..........aaaaaaaaaaaaaaaaaaaa 2093

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:     2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                 7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                 8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                 9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                             SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1541.8	73.7	1961	4	US-10-094-749-1437	Sequence 1437, Ap
2	1498.4	71.6	1597	3	US-09-774-528-9	Sequence 9, Appli
3	1498.4	71.6	1597	3	US-10-120-988-9	Sequence 9, Appli
4	467.4	22.3	2363	3	US-09-178-093B-25	Sequence 25, Appl
5	379.6	18.1	1455	4	US-10-154-419-93	Sequence 93, Appl
6	379.6	18.1	2397	4	US-10-154-419-91	Sequence 91, Appl
7	165.6	7.9	176	3	US-09-621-976-13903	Sequence 13903, A
8	120.6	5.8	1696	3	US-09-835-811-1	Sequence 1, Appli
9	120	5.7	3275	3	US-09-370-838-151	Sequence 151, App
10	120	5.7	3275	3	US-09-854-133-151	Sequence 151, App
11	119.4	5.7	882	3	US-09-311-021-107	Sequence 107, App
12	119.2	5.7	1459	3	US-09-537-654-3	Sequence 3, Appli
13	119.2	5.7	1459	5	US-10-818-809-3	Sequence 3, Appli
14	118.6	5.7	674	3	US-09-620-405B-465	Sequence 465, App
15	118.6	5.7	674	3	US-09-433-826B-465	Sequence 465, App
16	118.6	5.7	674	3	US-09-604-287A-465	Sequence 465, App
17	118.6	5.7	674	3	US-09-834-759-465	Sequence 465, App
18	118.6	5.7	674	3	US-09-590-751A-465	Sequence 465, App

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rng.

Score Home Page | **Retrieve Application List** | **SCORE System Overview** | **SCORE FAQ** | **Comments / Suggestions**

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rng.

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```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          August  7, 2006, 14:03:26 ; Search time 1150 Seconds
                                             (without alignments)
                                             4328.857 Million cell updates/sec

Title:           US-10-679-362-2
Perfect score:   2469
Sequence:        1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:       10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113044_25898/app_query.fasta_1
-DB=N_Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06p
-USER=US10679362_@CGN_1_1_1147_@runat_07082006_113044_25898 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       N_Geneseq_8:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
                            SUMMARIES
Result           Query
```

```
No.    Score  Match Length DB   ID                       Description
--------------------------------------------------------------------------
  1    2469   100.0   1597  8   ABX70783                 Abx70783 Novel hum
  2    2469   100.0   2057  8   ABZ80236                 Abz80236 Human tra
  3    2469   100.0   2093 10   ADF90163                 Adf90163 cDNA enco
  4    2469   100.0   2093 13   ADR03798                 Adr03798 Human cDN
  5    2469   100.0   5821 14   ADZ49865                 Adz49865 Insulin s
  6    2466    99.9   2807  8   ABX12019                 Abx12019 Transport
  7    2460    99.6   1501 10   ABX70643                 Abx70643 Human cDN
  8   2402.5    97.3  3114  6   AAL44674                 Aal44674 Human tra
  9    2398    97.1   1513 10   ABX70642                 Abx70642 Human cDN
 10    2324    94.1   1428  4   ABL57930                 Abl57930 Human VG5
 11    2217    89.8   1961 10   ADA53869                 Ada53869 Human cod
 12    2217    89.8   1961 13   ADS10331                 Human the
 13   2146.5    86.9  1824  8   ABZ80241                 Abz80241 Rat LYAAT
 14   2144.5    86.9  1625  8   ABZ80238                 Abz80238 Mouse tra
 15   2142.5    86.8  1784  4   ABL57913                 Abl57913 Rat VG51
 16    1959    79.3   1889  4   ABL57912                 Abl57912 Rat VG41
 17   1722.5    69.8  1619  6   ABQ79491                 Abq79491 Human HIP
 18   1722.5    69.8  3434  8   ABZ80230                 Abz80230 Human tra
 19   1718.5    69.6  1464  6   AAD44327                 Aad44327 Human tra
 20   1718.5    69.6  1593 13   ADN33180                 Adn33180 Human tra
 21   1718.5    69.6  2142  8   AAD47354                 Aad47354 Human tra
 22   1713.5    69.4  2444 12   ADQ63759                 Adq63759 Novel hum
 23   1678.5    68.0  2421  8   ABZ80228                 Abz80228 Rat tramd
 24   1551.5    62.8  2108 12   ADJ27245                 Adj27245 Human TRI
 25    1544    62.5   1520  6   ABQ79492                 Abq79492 Human HIP
 26    1539    62.3   2083 12   ADJ27264                 Adj27264 Human TRI
 27   1476.5    59.8  1703  8   ABZ80231                 Abz80231 Human tra
 28   1476.5    59.8  2456 13   ADR07759                 Adr07759 Full leng
 29    1463    59.3   1299 12   ADP28269                 Adp28269 Human·sec
 30    1461    59.2   1293 12   ADP28425                 Adp28425 Human sec
 31   1452.5    58.8  1473  6   AAD41820                 Aad41820 Human tra
 32    1420    57.5   1752  8   ABZ80237                 Abz80237 Mouse tra
 33   1375.5    55.7  1557 13   ADS10330                 Human the
 34   1333.5    54.0   947   5   ABV23244                 Abv23244 Human pro
 35   1333.5    54.0   947   5   ABV29088                 Abv29088 Human pro
 36    1301    52.7   3558 12   ADQ67469                 Adq67469 Novel hum
 37   1293.5    52.4  3573  4   ABL57910                 Abl57910 Rat VG1 c
 38    1263    51.2    953 10   ABX70644                 Abx70644 Human cDN
 39    1263    51.2   1098 13   ADS11640                 Ads11640 Human the
 40    1263    51.2   1098 13   ADS11639                 Ads11639 Human the
 41   1255.5    50.9  1455 10   ADD37512                 Add37512 Human tra
 42   1255.5    50.9  2366  4   AAI59840                 Aai59840 Human pol
 43   1255.5    50.9  2397  8   ABV72444                 Abv72444 Nucleotid
 44   1255.5    50.9  2397 10   ADD37510                 Add37510 Human tra
 45   1255.5    50.9  2423  4   AAI58054                 Aai58054 Human pol
```

ALIGNMENTS

RESULT 1
ABX70783
ID   ABX70783 standard; cDNA; 1597 BP.
XX
AC   ABX70783;
XX
DT   05-MAR-2003 (first entry)
XX
DE   Novel human cDNA sequence #8.
XX
KW   Human; gene; ss; nervous system disorder; peripheral neuropathy;
KW   Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
KW   neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
KW   autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
KW   insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
KW   ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
KW   fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
KW   coagulation disorder; cancer; tumour; inflammatory disease; septic shock;
KW   Crohn's disease; anaphylaxis; proliferation; chemotactic;
KW   differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
KW   haemostatic; antiinflammatory; expressed sequence tag; EST.
XX
OS   Homo sapiens.
XX
PN   WO200281731-A2.
XX
PD   17-OCT-2002.
XX
PF   29-JAN-2002; 2002WO-US001222.
XX
PR   30-JAN-2001; 2001US-00774528.
XX
PA   (HYSE-) HYSEQ INC.
PA   (GOOD/) GOODRICH R W.
XX
PI   Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI   Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR   WPI; 2003-058563/05.
XX

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rst.

Score Home Page   Retrieve Application List   SCORE System Overview   SCORE FAQ   Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rst.

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```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:         August  7, 2006, 14:31:09 ; Search time 6639 Seconds
                                           (without alignments)
                                           6013.918 Million cell updates/sec

Title:          US-10-679-362-2
Perfect score:  2469
Sequence:       1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:     96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113047_25946/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10679362_@CGN_1_1_6323_@runat_07082006_113047_25946 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      EST:*
                 1:  gb_est1:*
                 2:  gb_est3:*
                 3:  gb_est4:*
                 4:  gb_est5:*
                 5:  gb_est6:*
                 6:  gb_htc:*
                 7:  gb_est2:*
                 8:  gb_est7:*
                 9:  gb_est8:*
                10:  gb_est9:*
                11:  gb_gss1:*
                12:  gb_gss2:*
                13:  gb_gss3:*
                14:  gb_gss4:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                         SUMMARIES
                  %
Result          Query
  No.    Score Match Length DB  ID                      Description
```

SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rge.

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rge.

start

```
                        GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on:        August  7, 2006, 14:09:14 ; Search time 8148 Seconds
                                          (without alignments)
                                          5603.640 Million cell updates/sec

Title:         US-10-679-362-2
Perfect score: 2469
Sequence:      1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters:      12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113045_25911/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss04
-USER=US10679362_@CGN_1_1_5548_@runat_07082006_113045_25911 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     GenEmbl:*
               1:  gb_env:*
               2:  gb_pat:*
               3:  gb_ph:*
               4:  gb_pl:*
               5:  gb_pr:*
               6:  gb_ro:*
               7:  gb_sts:*
               8:  gb_sy:*
               9:  gb_un:*
               10:  gb_vi:*
               11:  gb_ov:*
               12:  gb_htg:*
               13:  gb_in:*
               14:  gb_om:*
               15:  gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
                    %
Result          Query
```

```
No.    Score   Match Length DB    ID                          Description
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   1    2469   100.0   1597   2   AR541761                    AR541761 Sequence
   2    2469   100.0   1597   2   AR698923                    AR698923 Sequence
   3    2469   100.0   1710   5   AY162213                    AY162213 Homo sapi
   4    2469   100.0   5823   5   HSM806092                   BX537963 Homo sapi
   5    2460    99.6   1501   2   AX717763                    AX717763 Sequence
   6    2439    98.8   2028   5   AB168788                    AB168788 Macaca fa
   7    2438    98.7   5585   5   AF516142                    AF516142 Homo sapi
   8  2402.5    97.3   3114   2   AX686980                    AX686980 Sequence
   9    2398    97.1   1513   2   AX717761                    AX717761 Sequence
  10    2324    94.1   1428   2   AX049362                    AX049362 Sequence
  11  2317.5    93.9   2296  14   AY989816                     AY989816 Oryctolag
  12    2217    89.8   1961   2   AX714753                    AX714753 Sequence
  13    2217    89.8   1961   5   AK057340                    AK057340 Homo sapi
  14  2146.5    86.9   1824   6   AF361239                    AF361239 Rattus no
  15  2142.5    86.8   1784   2   AX049344                    AX049344 Sequence
  16  2141.5    86.7   1611   6   AF453743                    AF453743 Mus muscu
  17  2137.5    86.6   2034   6   AY211262                    AY211262 Mus muscu
  18    2029    82.2   1402   5   AY227111                    AY227111 Homo sapi
  19    1959    79.3   1889   2   AX049343                    AX049343 Sequence
  20  1722.5    69.8   2140   5   BC101103                    BC101103 Homo sapi
  21  1722.5    69.8   2142   5   BC101101                    BC101101 Homo sapi
  22  1718.5    69.6   1464   2   AX555035                    AX555035 Sequence
  23  1718.5    69.6   2142   2   AX575471                    AX575471 Sequence
  24  1713.5    69.4   2444   2   CQ842273                    CQ842273 Sequence
  25  1713.5    69.4   2444   5   AK122630                    AK122630 Homo sapi
  26  1711.5    69.3   3407   5   AY162214                    AY162214 Homo sapi
  27  1700.5    68.9   2420   6   BC044800                    BC044800 Mus muscu
  28  1697.5    68.8   2357   6   AF453744                    AF453744 Mus muscu
  29  1697.5    68.8   2456   6   AF512429                    AF512429 Mus muscu
  30  1689.5    68.4   2767  11   BC070857                     BC070857 Xenopus 1
  31  1678.5    68.0   2436   6   AF512430                    AF512430 Rattus no
  32    1623    65.7    925   2   CQ728082                    CQ728082 Sequence
  33    1592    64.5   1420   5   AY227112                    AY227112 Homo sapi
  34  1556.5    63.0   2057   5   BC101102                    BC101102 Homo sapi
  35  1515.5    61.4   2156   5   BC101100                    BC101100 Homo sapi
  36  1476.5    59.8   1597   5   BC101095                    BC101095 Homo sapi
  37  1476.5    59.8   2268   5   AY162215                    AY162215 Homo sapi
  38  1476.5    59.8   2456   2   CQ850796                    CQ850796 Sequence
  39  1476.5    59.8   2456   5   AK127978                    AK127978 Homo sapi
  40  1472.5    59.6   1597   5   BC101094                    BC101094 Homo sapi
  41  1452.5    58.8   1473   2   AX571858                    AX571858 Sequence
  42  1450.5    58.7   1751   6   BC097463                    BC097463 Rattus no
  43    1447    58.6   1720   5   BC101092                    BC101092 Homo sapi
  44    1447    58.6   1720   5   BC101093                    BC101093 Homo sapi
  45    1420    57.5   1752   6   AY211261                    AY211261 Mus muscu
```

                              ALIGNMENTS

```
RESULT 1
AR541761
LOCUS       AR541761                 1597 bp     DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 9 from patent US 6743619.
ACCESSION   AR541761
VERSION     AR541761.1  GI:53933841
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1597)
  AUTHORS   Tang,Y.T., Zhou,P., Goodrich,R., Liu,C., Asundi,V., Ren,F.,
            Zhang,J., Zhao,Q.A., Yang,Y., Xue,A.J., Wehrman,T., Wang,J.-R.,
            Wang,D. and Drmanac,R.T.
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: US 6743619-A 9 01-JUN-2004;
            Nuvelo; Sunnyvale, CA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1597
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              5.37e-247     Length:         1597
Score:                  2469.00       Matches:         476
Percent Similarity:     100.0%        Conservative:      0
Best Local Similarity:  100.0%        Mismatches:        0
Query Match:            100.0%        Indels:            0
DB:                     2             Gaps:              0

US-10-679-362-2 (1-476) x AR541761 (1-1597)

Qy      1 MetSerThrGlnArgLeuArgAsnGluAspTyrHisAspTyrSerSerThrAspValSer 20
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Db    103 ATGTCCACGCAGAGACTTCGGAATGAAGACTACCACGACTACAGCTCCACGGACGTGAGC 162

Qy     21 ProGluGluSerProSerGluGlyLeuAsnAsnLeuSerSerProGlySerTyrGlnArg 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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SCORE Search Results Details for Application 10679362 and Search Result us-10-679-362-2.p2n.rni.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10679362 and Search Result us-10-679-362-2.p2n.rni.

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OM protein - nucleic search, using frame_plus_p2n model

Run on:        August  7, 2006, 14:45:41 ; Search time 278 Seconds
                                          (without alignments)
                                          4805.654 Million cell updates/sec

Title:         US-10-679-362-2
Perfect score: 2469
Sequence:      1 MSTQRLRNEDYHDYSSTDVS..........YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext  0.5
               Ygapop 10.0 , Ygapext  0.5
               Fgapop  6.0 , Fgapext  7.0
               Delop   6.0 , Delext   7.0

Searched:      1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters:      2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10679362/runat_07082006_113049_25988/app_query.fasta_1
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abss03h -USER=US10679362_@CGN_1_1_204_@runat_07082006_113049_25988
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :     Issued_Patents_NA:*
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               3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
               4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
               5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
               6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
               7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
               8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
               9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
               10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2469	100.0	1597	3	US-09-774-528-9	Sequence 9, Appli
2	2469	100.0	1597	3	US-10-120-988-9	Sequence 9, Appli
3	2217	89.8	1961	4	US-10-094-749-1437	Sequence 1437, Ap